

FIG. 4

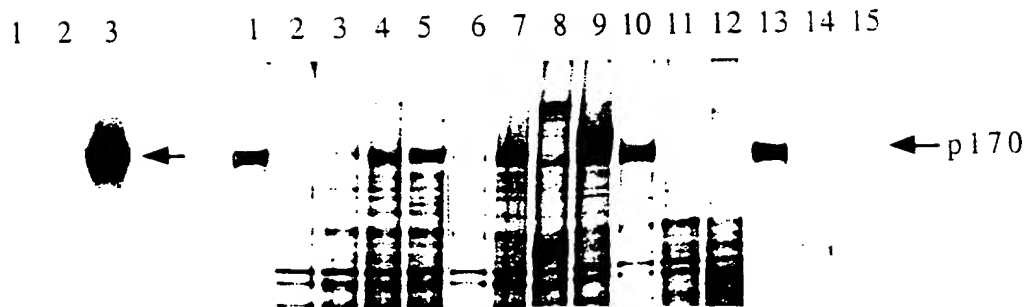


FIG. 5A

FIG. 5B

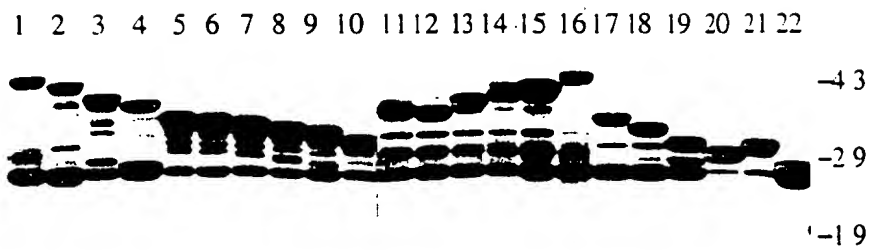


FIG. 7A

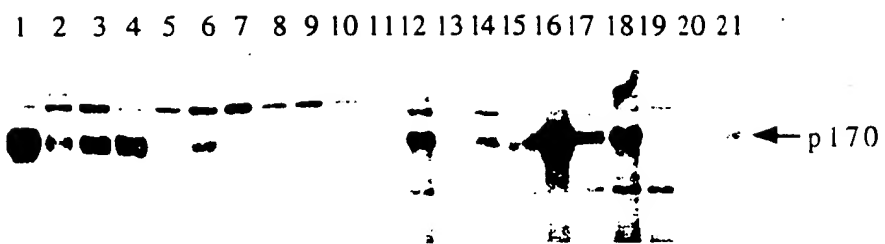


FIG. 7B

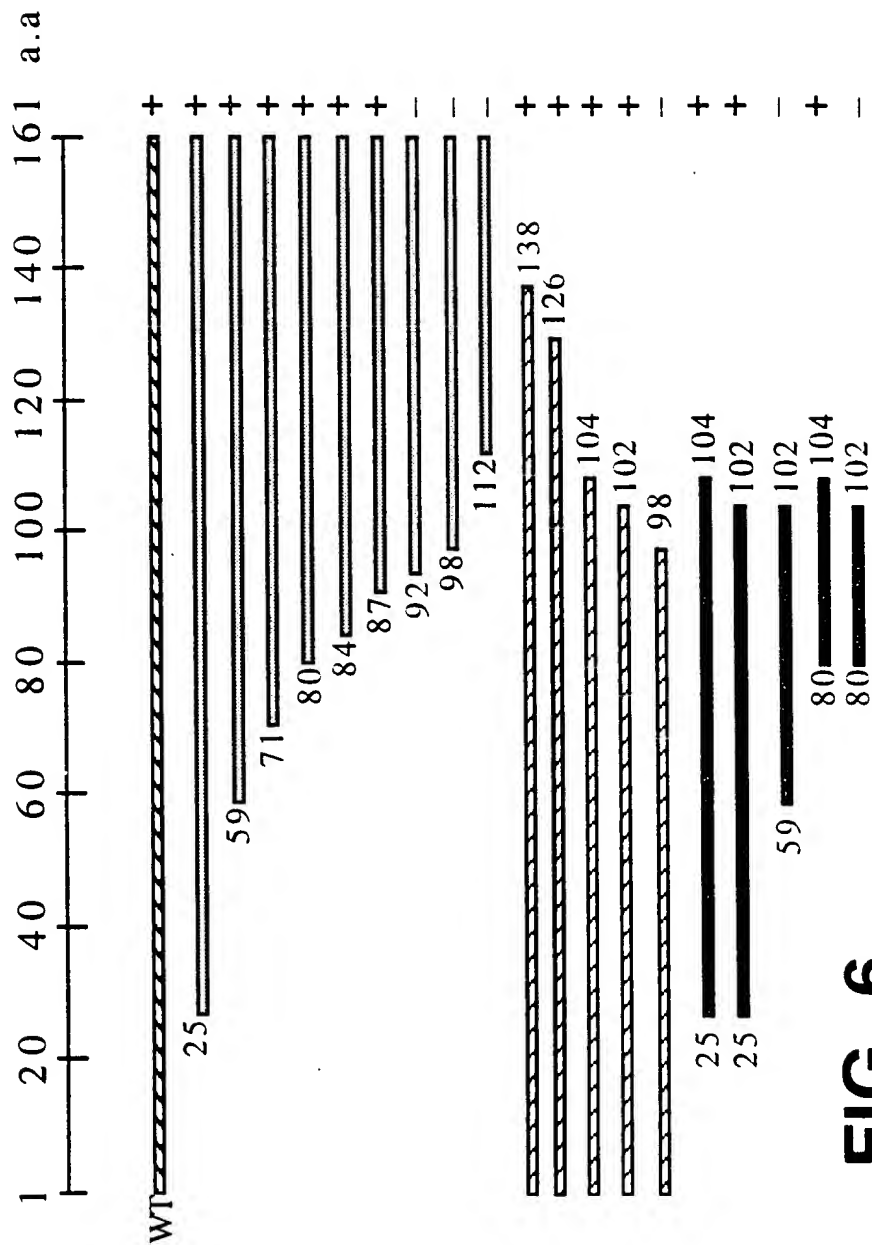


FIG. 6

DHBV pre-S region

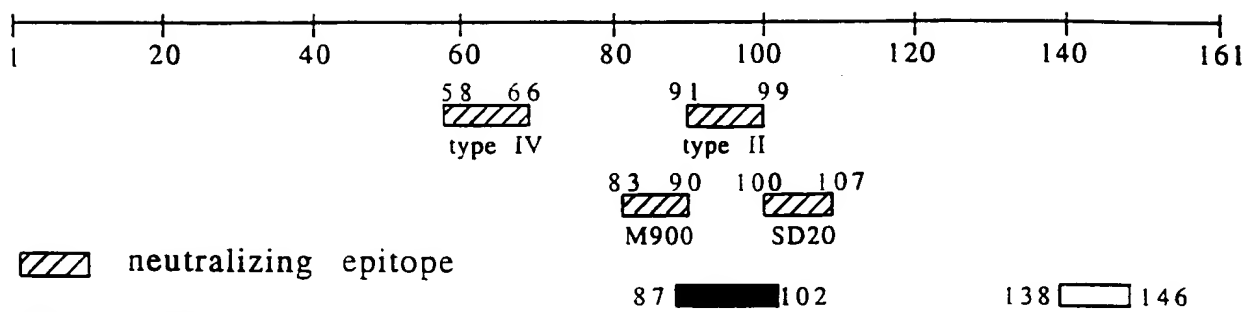


FIG. 8

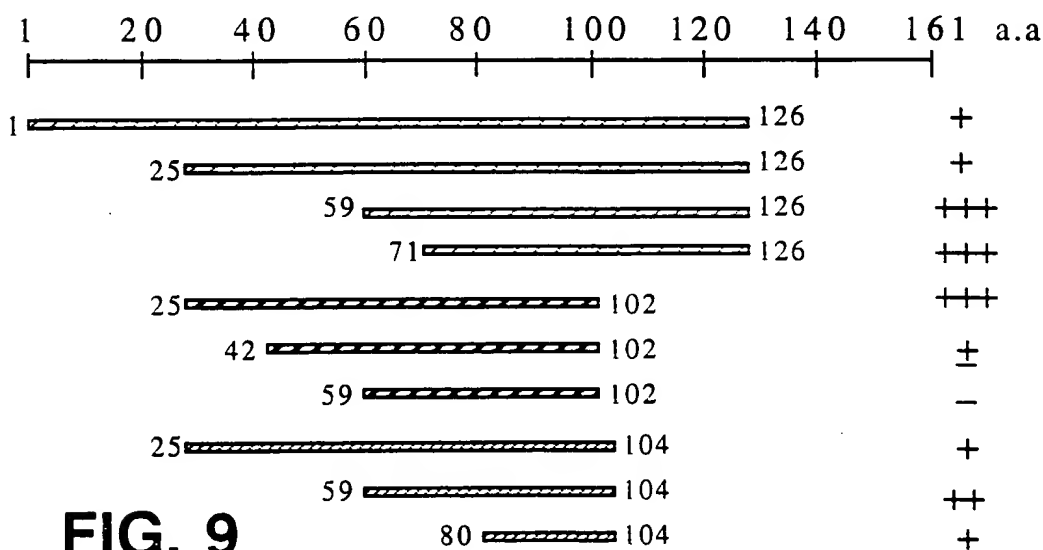


FIG. 9

1 2 3 4 5 6 7 8 9 10 11

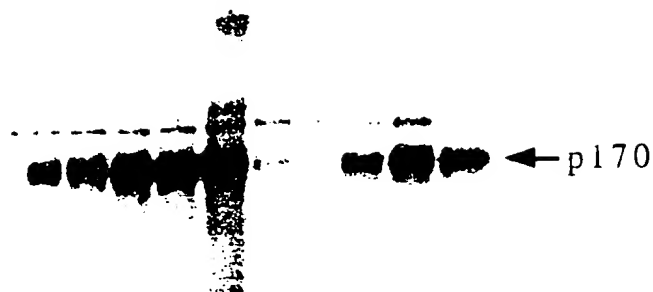


FIG. 10

A pre-S polypeptide containing p170 binding site blocks DHBV infectivity

1 2 3 4



FIG. 11

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

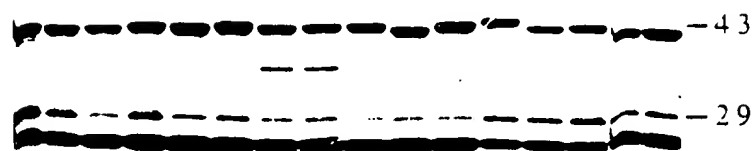


FIG. 13A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18



FIG. 13B

	87	90	93	96	99	102
wild-type	Q	W	T	P	E	E
W88S	S					
P90L		L				
E91G		G				
E92V			V			
D93F			F			
K95S				S		
R97L					L	
R97C					C	
E98A						A
E98V						V
R102G						G
E91G/K95S		G		S		
E91G/R97C		G			C	
K95S/A96T				S	T	
K95S/R97C				S		C
K95S/R97L/E98A				S	L	A

FIG. 12

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
peptide 3	LLSHEFQDETDTTEEETLYSAK (SEQ ID NO:21)
peptide 4	VEEGKVPVLNTPD (SEQ ID NO:22)

FIG. 14A

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
bovine CPH	.F.G...L.L.L.....P.....
human CPH	.F.G...L.I.L.....P.....
AEBP1 gene	KI.A.....D..L.....R
human CPN	...G.H...L.F..H..I..PL...V.
human CPM	..KG.N.W.LVVGRF.KE.RI.I....

peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
AEBP1 gene	.VQD...HL.....YEV.
bovine CPH	..HN...H.M.....
human CPN	..QD...H.L..M....YEV.
human CPM	..NS...H.M..M....
human CPH	..HS...H.M.....

FIG. 14B

[illegible]

N: G/A/T/C; X: A/G; Y: C/T; Z: G/T; V: A/C; W: A/T/C.

Primer sequences are written in small letters. For convenience antisense primers are written in the sense orientation.

FIG. 15

1/1
 ATG GGG CAA CAT CCA GCA AAA TCA ATG GAC GTC AGA CGG ATA GAA GGA GGA GAA ATA CTG
 M G Q H P A K S M D V R R I E G G E I L
 31/11
 61/21
 TTA AAC CAA CTT GCC GGA AGG ATG ATC CCA AAA GGG ACT TTG ACA TGG TCA GGC AAG TTT
 L N Q L A G R M I P K G T L T W S G K F
 91/31
 121/41
 CCA ACA CTA GAT CAC GTG TTA GAC CAT GTG CAA ACA ATG GAG GAG ATA AAC ACC CTC CAG
 P T L D H V L D H V Q T M E E I N T L Q
 151/51
 181/61
 AAT CAG GGA GCT TGG CCT GCT GCG GGA AGG AGA GTA GGA TTA TCA AAT CCG ACT CCT
 N Q G A W P A G A G R R V G L S N P T P
 211/71
 241/81
 CAA GAG ATT CCT CAG CCC CAG TGG ACT CCC GAG GAA GAC CAA AAA GCA CGC GAA CCT TTT
 Q E I P Q P Q W T P E E D Q K A R E A F
 271/91
 301/101
 CGC CGT TAT CAA GAA AGA CCA CCG GAA ACC ACC ATT CCT CCG TCT TCC CCT CCT
 R R Y Q E E R P P E T T I P P S S P P
 331/111
 361/121
 CAG TGG AAG CTA CAA CCC GGG GAC GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT
 Q W K L Q P G D D P L L G N Q S L L E T
 391/131
 421/141
 CAT CCG CTA TAC CAG TCA GAA CCA GCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG
 H P L Y Q S E P A V P V I K T P P L K K
 451/151
 481/161
 AAA
 K

FIG. 16

FIG. 17A

FIG. 17B

FIG. 17C

FIG. 17D

FIG. 17E

FIG. 17

(SEQ ID NO:)

AANQVG	VGA	FPRL	IPPH	GGIL	GWSP	QAQG	IL	TV	STIP	PPAS	IN	RO	SG	RO	PI	SP	PL	RD	SH	PQA	119
-Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(35)
-G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(36)
-GF	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(37)
-V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(38)
-DS	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(39)
-DS	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(40)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(41)
-D	-HK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(42)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(43)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(44)
-E	-IK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(45)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(46)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(47)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(48)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(49)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(50)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(51)
-E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(52)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(53)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(54)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(55)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(56)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(57)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(58)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(59)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(60)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(61)
-D	-K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(62)

FIG. 17B

[illegible]

GCAGAGCTAGACTCGTGGACTTCCTCAATTTCTAGGGGGAICTCCCGTGTGCTTGGCCAAATTCGCAGTCCCAACCTCCATCACCACCTCCGTGCTCTCAATTG	1
A-----G-A-----C-----	2
A-----A-G-A--AAG--C-----	3
-----G-----G-----G-----	4
A-----CTA--G--C-----C-----	5
A-----CTA--AG--C-----C-----	6

FIG. 17E

1/1	31/11
ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT	GAA GCA GGT GAG CCA GAG TTC AAG TAT ATT
M E I S D N P G V H	E A G E P E F K Y I
61/21	91/31
GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG	CGA GAG CTG CTC CTG AAC CTC ATC GAG TAC
G N M H G N E V V G	R E L L L N L I E Y
121/41	151/51
CTC TGC AAG AAC TTC GGC ACA GAT CCC GAA	GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC
L C K N F G T D P E	V T D L V Q S T R I
181/61	211/71
CAC ATC ATG CCG TCC ATG AAC CCA GAT GGC	TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA
H I M P S M N P D G	Y E K S Q E G D R G
241/81	271/91
GGC ACC GTT GGC AGA AAT AAC AGC AAC AAC	TAC GAC CTG AAC CGG AAC TTC CCA GAT CAG
G T V G R N N S N N	Y D L N R N F P D Q
301/101	331/111
TTC TTC CAG GTG ACA GAC CCT CCG CAG CCA	GAA ACT CTT GCT GTC ATG AGC TGG TTG AAA
F F Q V T D P P Q P	E T L A V M S W L K
361/121	391/131
ACT TAC CCG TTC GTG CTT TCA GCA AAC CTG	CAT GGA GGT TCT CTG GTG GTT AAT TAC CCT
T Y P F V L S A N L	H G G S L V V N Y P
421/141	451/151
TTT GAT GAC GAT GAA CAA GGA ATA GCC ATA	TAC AGT AAA TCC CCA GAC GAT GCT GTG TTT
F D D D E Q G I A I	Y S K S P D D A V F
481/161	511/171
CAG CAG CTG GCA CTT TCC TAC TCC AAG GAA	AAC AAA AAG ATG TAT CAG GGA AGC CCT TGT
Q Q L A L S Y S K E	N K K M Y Q G S P C
541/181	571/191
AAG GAT TTG TAC CCC ACA GAG TAC TTT CCA	CAT GGC ATC ACG AAC GGG GCC CAG TGG TAC
K D L Y P T E Y F P	H G I T N G A Q W Y
601/201	631/211
AAC GTT CCA GGT GGG ATG CAG GAC TGG AAT	TAC TTA AAT ACC AAC CTG TTT GAA GTG ACC
N V P G G M Q D W N	Y L N T N L F E V T
661/221	691/231
ATT GAG CTG GGC TGT GTG AAA TAC CCA AAA	GCA GAG GAG CTG CCG AAG TAC TGG GAG CAG
I E L G C V K Y P K	A E E L P K Y W E Q
721/241	751/251
AAC CGT AGA TCT CTC CTC CAG TTC ATT AAA	CAG GTT CAC CGC GGC ATC TGG GGA TTT GTG
N R R S L L Q F I K	Q V H R G I W G F V
781/261	811/271
CTG GAT GCC ACG GAC GGA AGG GGC ATT CTC	AAC GCC ACC ATC AGC GTC GCC GAC ATC AAC
L D A T D G R G I L	N A T I S V A D I N
841/281	871/291
CAC CCC GTG ACC ACC TAC AAA GAT GGG GAC	TAC TGG CGC CTC TTG GTC CAG GGG ACG TAC
H P V T T Y K D G D	Y W R L L V Q G T Y
901/301	931/311
AAA GTC ACA GCA TCT GCC CGA GGG TAT GAT	CCA GTC ACT AAA ACG GTG GAA GTC GAC AGC
K V T A S A R G Y D	P V T K T V E V D S
961/321	991/331
AAA GGT GGG GTG CAG GTC AAC TTC ACT CTT	TCA CGG ACA GAC GCC AAA GTG GAG GAG GGG
K G G V Q V N F T L	S R T D A K V E E G
1021/341	1051/351
AAG GTG CCA GTC CTG AAC ACC CCA GAC ACC	AGC GAC CCC AAC GAG AAG GAG TTT GAG ACT
K V P V L N T P D T	S D P N E K E F E T
1081/361	1111/371
CTG ATC AAA GAT CTA TCT GCT GAA AAC GGC	CTG GAG (SEQ ID NO:63)
L I K D L S A E N G	L E (SEQ ID NO:64)

FIG. 18

1/1 31/11
 TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC CTT AAT GAA GGC
 F V Q D K S G K A I S K A T I V L N E G
 61/21 91/31
 TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT GTG CTG TTG GCT CCT GGT TTG CAT
 L R V Y T K E G G Y F H V L L A P G L H
 121/41 151/51
 AAC ATC AAT GCG ATA GCG GAT GGG TAC CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC
 N I N A I A D G Y Q Q K H M K V L V R H
 181/61 211/71
 GAT GCA CCC AGC TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT
 D A P S S V F M V F D M E N R I F G L P
 241/81 271/91
 CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC CTC ACT GCC TGT
 R E L V V T V A G A I M S A L V L T A C
 301/101 331/111
 ATC ATC TGG TGT GTC TCA ATC AAG GCC AAC AGA CAC AAA GAT GGC TTC CAC TGC CGG
 I I W C V C S I K A N R H K D G F H C R
 361/121 391/131
 CAG CAC CAC GAT TAC GAG GAC GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC
 Q H H D D Y E D E I R M M S T G S K K S
 421/141 451/151
 CTT TTG AGC CAC GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA (SEQ ID NO:65)
 L L S H E F Q D E T D T E E (SEQ ID NO:66)

FIG. 19

HBV (SEQ ID NO:67)
DHBV (SEQ ID NO:68)

71	HBV	H	G	G	I	L	G	W	S	P	Q	A	Q	G	I	L	T	V	S	T	I	P	P	P	A	S	T	N	R	Q	S	G	R	Q	P	T	P	I	S	P	P	L	R	D	S	H	P	Q	118
69	DHBV	A	G	R	R	V	G	L	S	N	P	T	P	Q	E	I	P	Q	P	Q	W	T	P	E	E	D	Q	K	A	R	E	A	F	R	R	Y	Q	E	E	R	P	P	E	T	T	I	P	P	116
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		

HBV (SEQ ID NO:67)
DHBV (SEQ ID NO:68)

p170 binding site

FIG. 20

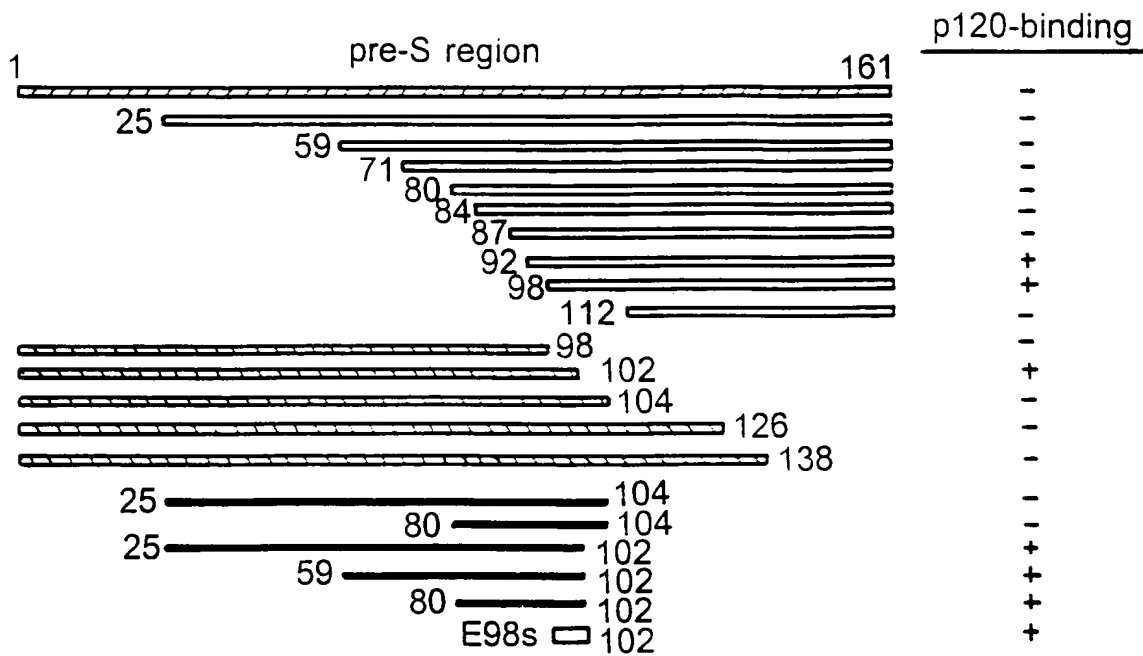


FIG. 21A

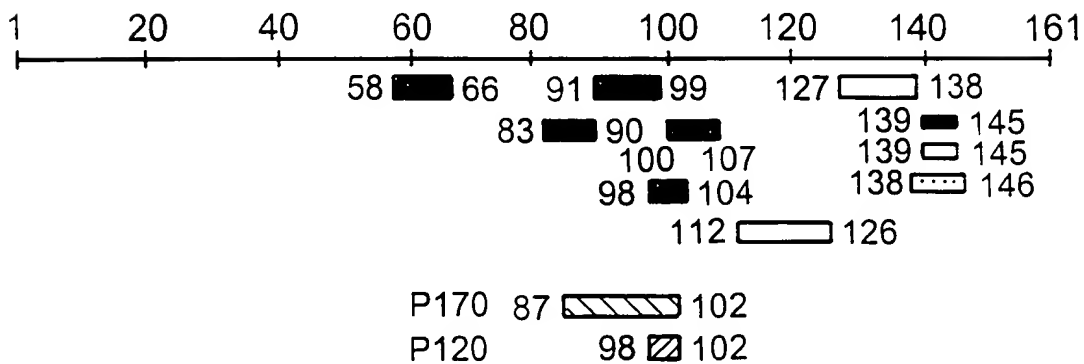


FIG. 22

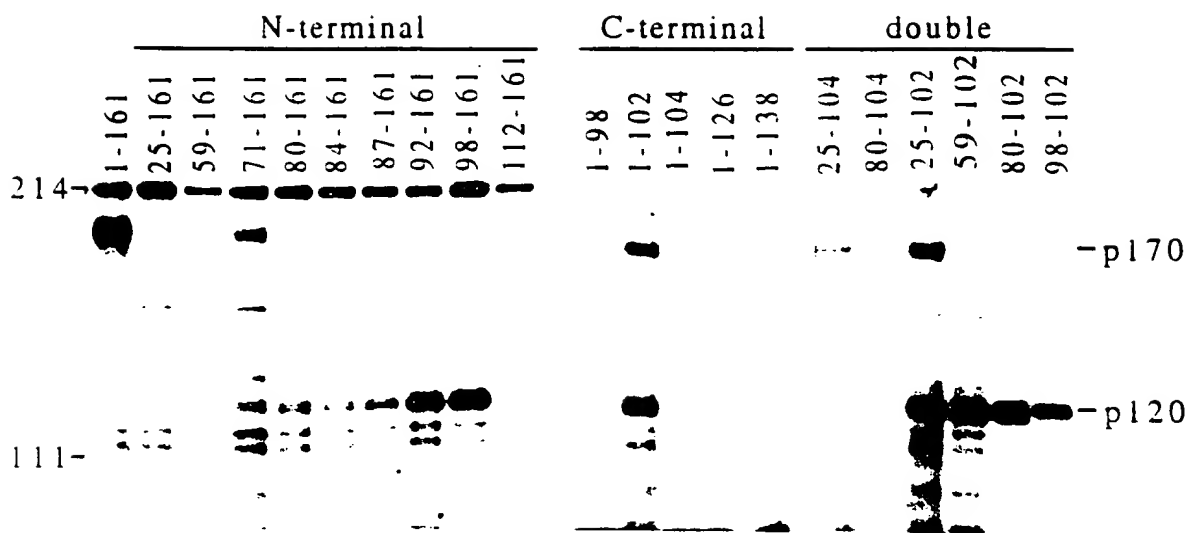


FIG. 21B

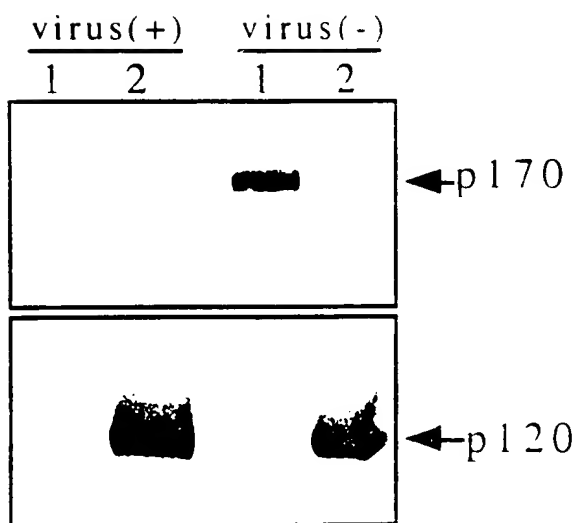


FIG. 23

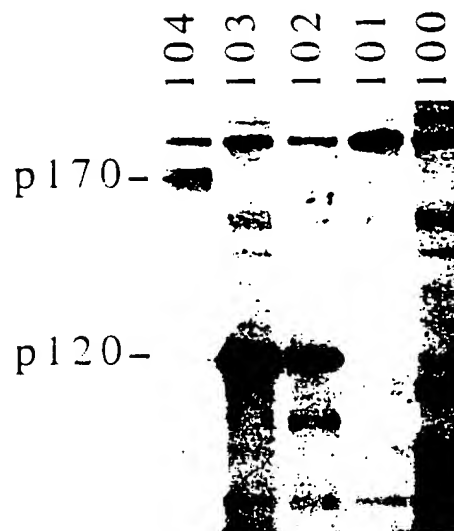


FIG. 24

			97	98	99	100	101	102	<u>p120-binding</u>
WT	Lys	Ala	Arg	Glu	Ala (Tyr)	Phe	Arg	Arg	+
R97C			Cys						+
E98V				Val					+
E98A				Ala					+
A99D					Asp				+
F100V						Val			-
F100L						Leu			-
F100W						Trp			+
R101L							Leu		-
R101H							His		-
R101K							Lys		+ weak
R102G								Gly	-
R102H								His	-
R102K								Lys	-

FIG. 25A

peptide 1: DVSGVLFQYPDTEGK (SEQ ID NO:70)

peptide 2: EVYRLALQTREQHIRRD (SEQ ID NO:71)

peptide 3: SGAQGEYAGLA-AIK (SEQ ID NO:72)

peptide 4: IQPIEVDK (SEQ ID NO:73)

Peptide sequences of p120.

FIG. 30

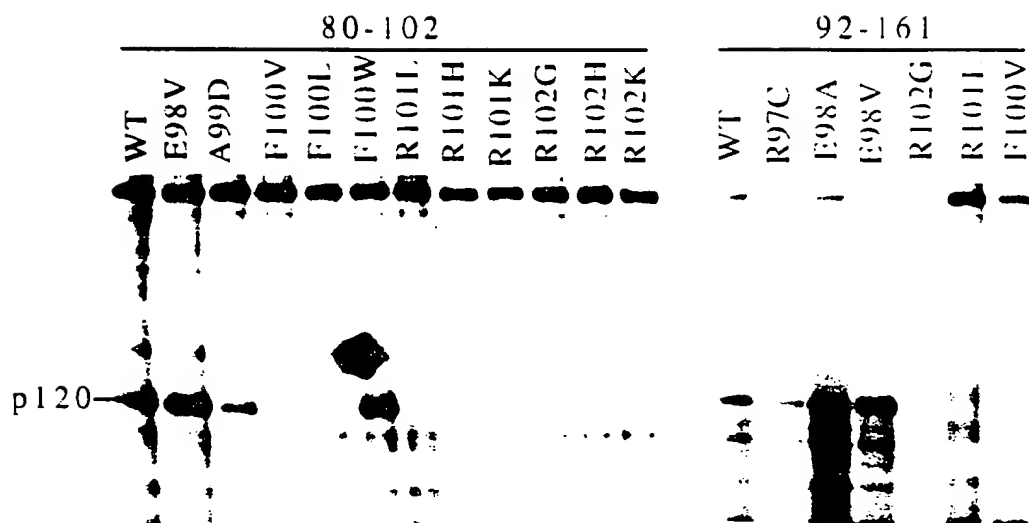


FIG. 25B

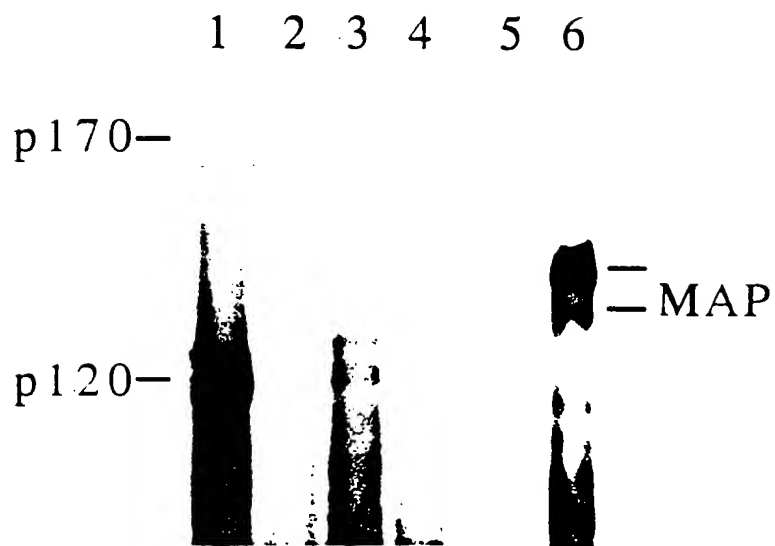


FIG. 26

1 2 3 4 5 6

FIG. 27A

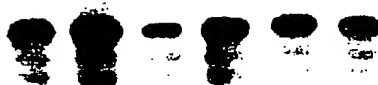


FIG. 27B



FIG. 27C



FIG. 27D



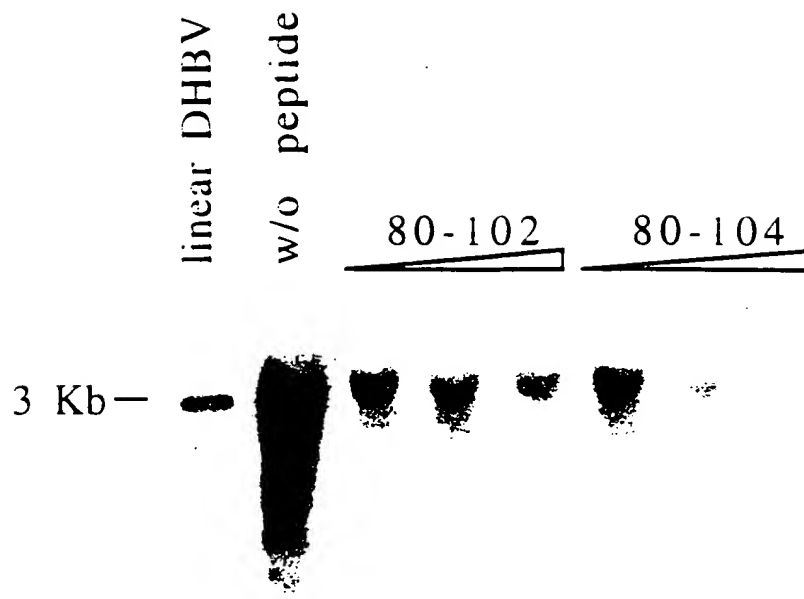


FIG. 28

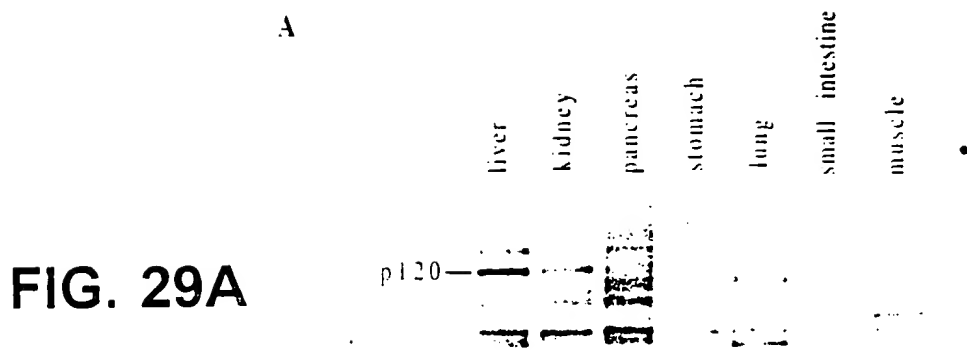


FIG. 29A

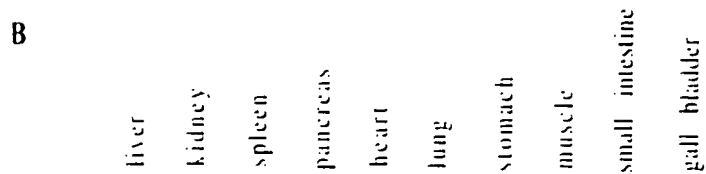


FIG. 29B

1/1
 GAG CGG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT GAC TTC TCC CGG CCG CAC
 E A A R C I E Q L L P R H D D F S R R H
 61/21
 ATC GGC CCC GAG GAG GGG GAG AAG AGG GAG ATG CTG CGA GCC CTC GGG GTG CAG AGC GTC
 I G P R E G E K R E M L R A L G V Q S V
 121/41
 GAG GAG CTG ATG GAT AAA GCC ATC CCG GGC AGC AGC CTG GGC AGG CCG CTG AGG ATG
 E E L M D K A I P G S I R L R R P L R M
 181/61
 GAG GAC CCC GTG GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT AAT GCA AGC AAG AAC
 E D P V G G E N E I L E T L Y N I A S K N
 241/81
 AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG CCT CAA CCC ATT
 K I W R S Y I G M G Y Y N C S V P Q P I
 301/101
 GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC CAG TAT ACT CCC TAC CAA CCT GAG
 A R N L L E N A G W V T Q Y T P Y Q P E
 361/121
 GTC TCA CAG GGC AGG CTG GAG AGC CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA
 V S Q G R L E S L L N Y Q T M V C D I T
 421/141
 CGA ATG GAT GTG GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG
 G M D V A N A S L L D E G T A A A E A M
 481/161
 CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC CGA TGC CAC CCT
 Q L C H R H N K R R K F Y V D S R C H P

FIG. 31A

541/181 571/191
 CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT ACA GGT GTT ATT ACT GAG CTC AAA
 Q T I A V V Q T R A N Y T G V I T E L K
 601/201 631/211
 TTA CCC CAT GAG ATG GAT TTC AGT GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA
 L P H E M D F S G K D V S G V L F Q Y P
 661/221 691/231
 GAC ACT GAG GGG AAG GTG GAA GAC TTC TCT GAA CTT GTT GAA AGA GCT CAT CAG AAC GGG
 D T E G K V E D F S E L V E R A H Q N G
 721/241 751/251
 ACT CTT GCC TGC TGT GCT ACT GAT CTT CTG GCT CTC TGT ATT CTG AAG CCT CCT GGA GAG
 T L A C C A T D L L A L C I L K P P G E
 781/261 811/271
 TTT GGG GTA GAT GTT GTC CTG GGT AGC TCC CAG AGA TTT GGT GTG CCA CTC TGC TAT GGG
 F G V D V V L G S S Q R F G V P L C Y G
 841/281 871/291
 GGA CCC CAC GCA GCA TTC TTC GCT GTC AAG GAA AAC CTA GTG AGA ATG ATG CCA GGC AGG
 G P H A A F F A V K E N L V R M M P G R
 901/301 931/311
 ATG GTG GGT GTC ACA AGA GAT GCA AAT GGA AAA GAA GTT TAC CGA CTG GCT TTA CAA ACA
 M V G V T R D A N G K E V Y R L A L Q T

FIG. 31B

961/321 CGA GAG CAG CAT ATC AGG AGG GAC AAA GCT ACA AGC AAC ATC TGC ACA GCA CAG GCT CTT
 R E Q H I R R D K A T S N I C T A Q A L
 1021/341 CTG GCT AAT ATG GCA GCC ATG TTT GGT GTC TAC CAT GCG TCT GAT GGA TTA AGG GAT ATT
 L A N M A A M F G V Y H G S D G L R D I
 1081/361 GCA AGA CCG GTA CAC AAT GCT ACT TTA ATC CTG GCT GAA GGT CTC AGG AGA GCT GGT CAT
 A R R V H N A T L I L A E G L R R A G H
 1141/381 AAA CTG CAC CAT GAT CTG TTC TTT GAT ACC TTG ACA GTC ACG TGT GGA TGC TCA GTC AAA
 K L H H D L F F D T L T V T C G C S V K
 1201/401 GAA GTT TTG GAC AGG GCA GCT CTG AGA AAG ATA AAT TTT CGC ATT TAT AGT GAT GCC AGA
 E V L D R A A L R K I N F R I Y S D G R
 1261/421 CTT GCA GTA TCA CTT GAT GAA ACT GTA AGT GAG AAA GAC CTA GAT GAC ATA TTA TGG ATT
 L G V S L D E T V S E K D L D D I L W I
 1321/441 TTT GGT TGC GAG TCT TCA GCT GAA CTA ATT GCT GAA GGT ATG GGC GAG GAA ACC AAA GGT
 F G C E S S A E L I A E G M G E E T K G
 1381/461 ATC CTT AGC ACC CCA TTT AAG AGA ACT TCC AAA TTC TTG ACC CAT CAG GTT TTC AAC AGC
 I L S T P F K R T S K F L T H Q V F N S

FIG. 31C

1441/481
 TAT CAC TCC GAA ACA AAT ATC GTA CGG TAC ATG AAG AGA TTA GAA AAC AAA GAT ATT TCC
 Y H S E T N I V R Y M K R L E N K D I S
 1501/501
 CTT GTT CAC AGC ATG ATT CCT TTG GGG TCC TGT ACA ATG AAG CTC AAT AGT TCA GCT GAA
 L V H S M I P L G S C T M K L N S S A E
 1561/521
 CTT GCA CCT ATT TCA TGG AAG GAA TTT GCC AAC ATC CAC CCC TTT GTG CCC TTG GAT CAA
 L A P I S W K E F A N I H P F V P L D Q
 1621/541
 GCT CAA GGG TAT CAG CAG CTT TTC AAG GAC TTA GAG AAG GAC CTG TGT GAG ATT ACT GGT
 A Q G Y Q Q L F K D L E K D L C E I T G
 1681/561
 TAC GAC AAA ATC TCC TTC CAA CCA AAC AGT GGA GCC CAA GGA GAG TAC GCA GGC TTG GCC
 Y D K I S F Q P N S G A Q G E Y A G L A
 1741/581
 GCA ATC AAA GCT TAT TTA AAT GCA AAA GGA GAA CGT CAT CGA AGT GTT TGC CTT ATT CCT
 A I K A Y L N A K G E R H R S V C L I P
 1801/601
 AGA TCT GCT CAT GGT ACA AAT CCA GCA AGT GCA CAG ATG GCA GGG ATG AAG ATT CAA CCA
 R S A H G T N P A S A Q M A G M K I Q P

FIG. 31D

1861/621	1891/631
GTT GAA GTA GAT AAA AAT GGG AGC ATT GAT ATC TCC CAT TTA AAA GCA ATG GTG GAC AAA	
V E V D K N G S I D I S H L K A M V D K	
1921/641	1951/651
CAC AAG GAG AAC CTG GCA GCC ATC ATG ATC ACA TAC CCT TCC ACC AAT GGT GTG TTT GAG	
H K E N L A A I M I T Y P S T N G V F E	
1981/661	2011/671
GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA AAC GGA GGC CAG GTT TAC CTG GAT	
E E I G D V C E L I H K N G G Q V Y L D	
2041/681	2071/691
GGA GCA AAC ATG AAC GCC CAA GTG GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC	
G A N M N A Q V G L C R P G D Y G S D V	
2101/701	2131/711
TCT CAC TTA AAC CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA CCT GGA ATG	
S H L N L H K T F C I P H G G G P G M	
2161/721	2191/731
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT CCT GTC ATC AAG	
G P I G V K K H L A P Y L P T H P V I K	

FIG. 31E

2221/741
ATT CAG ACG GAT AAG GAT GCA TGT CCT TTG GGT ACT GTC AGT GCT GCA CCT TGG GGT TCC
I Q T D K D A C P L G T V S A A P W G S

2281/761
AGT GCT ATA TTG CCT ATT TCC TGG GTG TAT ATC AAG ACA ATG CGA GCA AAG GGT CTT AAA
S A I L P I S W V Y I K T M G A K G L K

2341/781
CAC GCT TCT GAG GTT GCT ATA TTA AAT GCA AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC
H A S E V A I L N A N Y M A K R L E K H

2401/801
TAC AAA ATC CTT TTC AGA GGA GTA AGA GGT TAT GTA GCC CAT GAA TTC ATT TTG GAT ACA
Y K I L F R G V R G Y V A H E F I L D T

2461/821
AGA CCT TTC AAA ACA GCA AAC ATT GAA GCT GTG GAT CTT GCT AAG CGA CTT CAG GAT
R P F K K T A N I E A V D L A K R L Q D

2521/841
TAT GGT TTT CAT GCT CCA ACC ATG TCC TGG CCA GTG GCA GCC ACA CTT ATG ATT GAA CCA
Y G F H A P T M S W P V A G T L M I E P

2581/861
ACA GAG TCT GAA GAC AAG GCA GAG CTG GAC AGG TTT TGT GAT CCA ATG ATC AGT ATT CGA
T E S E D K A E L D R F C D A M I S I R

2251/751
GGT ACT GTC AGT GCT GCA CCT TGG GGT TCC
G T V S A A P W G S

2311/771
ATC AAG ACA ATG CGA GCA AAG GGT CTT AAA
I K T M G A K G L K

2371/791
AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC
N Y M A K R L E K H

2431/811
TAT GTA GCC CAT GAA TTC ATT TTG GAT ACA
Y V A H E F I L D T

2491/831
GCT GTG GAT CTT GCT AAG CGA CTT CAG GAT
A V D L A K R L Q D

2551/851
CCA GTG GCA GCC ACA CTT ATG ATT GAA CCA
P V A G T L M I E P

2611/871
TGT GAT CCA ATG ATC AGT ATT CGA
F C D A M I S I R

FIG. 31F

2641/881
 CAG GAA ATT GCT GAA ATA GAG GAG GGC AGG ATG GAC CCT CAG ATT AAC CCA TTA AAG ATG
 Q E I A E I E E G R M D P Q I N P L K M
 2701/901
 TCA CCA CAT ACT CTA AAC TGT GTC ACT TCT TCA AAG TGG GAT CGT CCT TAT TCC AGA GAA
 S P H T L N C V T S S K W D R P Y S R E
 2761/921
 GTG GCA GCA TTC CCA CTG CCG TTT GTG AAA CCT GAG AGC AAG TTT TGG CCC ACA ATT GCT
 V A A F P L P F V K P E S K F W P T I A
 2821/941
 CGC ATC GAT GAC ATA TAC GGA GAT CAA CAC CTG GTT TGT ACC TGC CCA CCG ATG GAA GCC
 R I D D I Y G D Q H L V C T C P P M E A
 2881/961
 TAC GAA TCT CCC TTC TCT GAA CAG AAG AGA GCA TCT TCG TAA (SEQ ID NO:74)
 Y E S P F S E Q K R A S S * (SEQ ID NO:75)

FIG. 31G